

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/566,851
Source: IFWP
Date Processed by STIC: 2/9/06

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IFM

RAW SEQUENCE LISTING

DATE: 02/09/2006

PATENT APPLICATION: US/10/566,851

TIME: 14:09:07

Input Set : A:\50304.112001.txt

Output Set: N:\CRF4\02012006\J566851.raw

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3 <110> APPLICANT: Jacquemin, Marc
4     Saint-Remy, Jean-Marie
6 <120> TITLE OF INVENTION: Variable antibodies
8 <130> FILE REFERENCE: 50304/112001
-> 10 <140> CURRENT APPLICATION NUMBER: US/10/566,851
-> 10 <141> CURRENT FILING DATE: 2006-02-01
10 <150> PRIOR APPLICATION NUMBER: GB 0319118.6
11 <151> PRIOR FILING DATE: 2003-08-14
13 <150> PRIOR APPLICATION NUMBER: GB 0319345.5
14 <151> PRIOR FILING DATE: 2003-08-18
16 <160> NUMBER OF SEQ ID NOS: 32
18 <170> SOFTWARE: PatentIn version 3.3
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21 <211> LENGTH: 496
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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29 <223> OTHER INFORMATION: KRIX-1 heavy chain variable region
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32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: (1)..(57)
34 <223> OTHER INFORMATION: nucleotide sequence encoding the leader sequence
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37 <221> NAME/KEY: misc_feature
38 <222> LOCATION: (133)..(192)
39 <223> OTHER INFORMATION: nucleotide sequence encoding CDR1
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42 <221> NAME/KEY: misc_feature
43 <222> LOCATION: (235)..(285)
44 <223> OTHER INFORMATION: nucleotide sequence encoding CDR2
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48 <222> LOCATION: (382)..(435)
49 <223> OTHER INFORMATION: nucleotide sequence encoding CDR3
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54 1              5              10              15
56 gcc cac tcc cag gtg caa ctg gtg caa tct ggg gct gag gtg aag aag      96
57 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
58              20              25              30

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60 cct ggg gcc tca gtg aag gtc tcc tgc aag acc tct gga tac aac ttc      144
61 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe
62      35      40      45
64 acc ggc tac tct gct tct gga cat atc ttc acc gcc tac tct gtg cac      192
65 Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His
66      50      55      60
68 tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga agg atc      240
69 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile
70 65      70      75      80
72 aac cct aac agt ggt gcc aca gac tat gca cat aaa ttt cag ggc agg      288
73 Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg
74      85      90      95
76 gtc acc atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg      336
77 Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu
78      100      105      110
80 agc agg ctg aca tct gac gac acg gcc atg tat tac tgt gcg aga gcc      384
81 Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala
82      115      120      125
84 gac aac tat ttc gat att gtg act ggc tat act tct cat tac ttt gac      432
85 Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp
86      130      135      140
88 tac tgg ggc cgg gga acc ctg gtc acc gtc tcc tca gcc tcc acc aag      480
89 Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
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92 ggc cca tcg gtc ttc c      496
93 Gly Pro Ser Val Phe
94      165
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108 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
109      20      25      30
112 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe
113      35      40      45
116 Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His
117      50      55      60
120 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile
121 65      70      75      80
124 Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg
125      85      90      95
128 Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu
129      100      105      110
132 Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala
133      115      120      125
136 Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp

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140 Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
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156 <222> LOCATION: (1)..(429)
157 <223> OTHER INFORMATION: KRIX-1 light chain variable region
159 <220> FEATURE:
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161 <222> LOCATION: (1)..(60)
162 <223> OTHER INFORMATION: nucleotide sequence encoding leader peptide
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166 <222> LOCATION: (130)..(164)
167 <223> OTHER INFORMATION: nucleotide sequence encoding CDR1
169 <220> FEATURE:
170 <221> NAME/KEY: misc_feature
171 <222> LOCATION: (211)..(231)
172 <223> OTHER INFORMATION: nucleotide sequence encoding CDR2
174 <220> FEATURE:
175 <221> NAME/KEY: misc_feature
176 <222> LOCATION: (328)..(357)
177 <223> OTHER INFORMATION: nucleotide sequence encoding CDR3
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182 1      5      10      15
184 gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct      96
185 Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser
186      20      25      30
188 ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt      144
189 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
190      35      40      45
192 gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa cct ggc cag gct      192
193 Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
194      50      55      60
196 ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca      240
197 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
198 65      70      75      80
200 cac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc      288
201 His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
202      85      90      95
204 agc aga ctg gag cct gaa gat ttt gca gtg tac tac tgt cag caa tat      336

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205 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
206          100          105          110
208 ggt acc tca gcc tta ctc act ttc ggc gga ggg acc aag gtg gag atc      384
209 Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
210          115          120          125
212 aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct      429
213 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
214          130          135          140
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218 <211> LENGTH: 143
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225 1          5          10          15
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229          20          25          30
232 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
233          35          40          45
236 Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
237          50          55          60
240 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
241 65          70          75          80
244 His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
245          85          90          95
248 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
249          100          105          110
252 Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
253          115          120          125
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263 <213> ORGANISM: Artificial Sequence
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275 <213> ORGANISM: Artificial Sequence
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Input Set : A:\50304.112001.txt

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287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
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313 <220> FEATURE:
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323 <213> ORGANISM: Artificial Sequence
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334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
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344 <210> SEQ ID NO: 12
345 <211> LENGTH: 37
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: Krix-1 reverse mutagenic primer Thr49Ala
352 <400> SEQUENCE: 12
353 ccagaagcag agtagccagc gaagttgtat ccagagg 37
356 <210> SEQ ID NO: 13
357 <211> LENGTH: 46
358 <212> TYPE: DNA

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/566,851

DATE: 02/09/2006

TIME: 14:09:08

Input Set : A:\50304.112001.txt

Output Set: N:\CRF4\02012006\J566851.raw

10 M:270 C: Current Application Number differs, Replaced Current Application No

10 M:271 C: Current Filing Date differs, Replaced Current Filing Date